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Using LISREL to Analyze Genetic and Environmental Covariance Structure

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A method is described in which the LISREL computer program is used for the genetic analysis of covariance structure. The method is illustrated with simulated and published twin data.

KEY WORDS: LISREL; genetic convariance; environmental covariance; twin data.

INTRODUCTION

Martin and Eaves (1977) developed a method for the analysis of genotypic and environmental covariance structure based on the work of Jöreskog (1973). Their method is a general approach to the analysis of covariance structure which allows simultaneous testing of hypotheses about the sources and structure of covariation. The method provides maximum-likelihood estimates of genetical and environmental factor loadings and specific variances. Martin and Eaves applied this method to twin data on cognitive abilities published by Loehlin and Vandenberg (1968). To obtain parameter estimates, standard errors of estimates, and chi-square tests, they implemented their method while using a minimization algorithm (EO4HAF) written by the Numerical Algorithms Group (1974). As their implementation—which is, in fact, a rather intricate affair—is not readily available, it would seem worthwhile to consider the possibility of handling their method by the LISREL computer program of Jöreskog and Sörbom (1981). The latter program is easily accessible and is widely known. In this paper we first show how LISREL can be used for the genetic analysis

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of covariance structure[3] and then proceed with some examples. We illustrate the use of LISREL for monozygotic (MZ) and dizygotic (DZ) twin data, but of course the method can be generalized to other cases as well. We used LISREL to replicate the analysis of twin data by Martin *et al.* (1981) on psychomotor performance during alcohol intoxication. We also applied LISREL to the data of Loehlin and Vandenberg and found that LISREL gave the same parameter estimates as obtained by Martin and Eaves.

USING LISREL

In this section we start with a concise description of the general LISREL-V model (Jöreskog and Sörbom, 1981). As we use the model in a somewhat nonstandard fashion, we at first refrain from substantial interpretations of the various components of the model and stick to a presentation that emphasizes a formal specification. Next, we consider the expressions for the expected contributions of the common and specific genetical and environmental factors to the matrices of mean products between and within twin pairs (Martin and Eaves, 1977) and show how this set of equations can be rewritten as a LISREL model. The interpretation of the various LISREL expressions then follows directly from these equations. In the closing part of this section, a completely worked example with simulated twin data is given.

THE LISTREL-V MODEL

Consider random vectors $\eta' = [\eta_1, \eta_2, \ldots, \eta_m]$ and $\xi' = [\xi_1, \xi_2, \ldots, \xi_n]$ of latent dependent and independent variables, respectively, and the following system of linear structural relations:

$$\eta = B\eta + \Gamma\xi + \zeta,$$

where $B(m \times m)$ and $\Gamma(m \times n)$ are coefficient matrices and $\zeta' = (\zeta_1, \zeta_2, \ldots, \zeta_m]$ is a random vector of residuals. The vectors xi and eta are not observed, but instead the vectors $y' = [y_1, y_2, \ldots, y_p]$ and $x' = [x_1, x_2, \ldots, x_q]$ are observed such that

$$y = \Lambda_y\eta + \epsilon,$$

$$x = \Lambda_x\xi + \delta,$$

where epsilon and delta are vectors of errors of measurement in y and x,

[3] Only after submitting this paper did we learn that a similar approach has been suggested by Fulker *et al.* (1983).

respectively. The matrices lambda-y ($p \times m$) and lambda-x ($q \times n$) are regression matrices of y on η and x on ξ. $\Phi(n \times n)$ and $\Psi(m \times m)$ are covariance matrices of ξ and ζ, and Θ_ϵ and Θ_δ are covariance matrices of ϵ and δ, respectively. The elements of Λ_y, Λ_x, B, Γ, Φ, Ψ, Θ_ϵ, and Θ_δ are are of three kinds:

(1) fixed parameters that have been assigned given values,
(2) constrained parameters that are unknown but equal to one or more other parameters, and
(3) free parameters that are unknown and not constrained to be equal to any other parameters.

LISREL ANALYSIS OF TWIN DATA

The expected contributions of the common and specific genetical and environmental factors to the matrices of mean products between and within twin pairs can be written as follows (Martin and Eaves, 1977):

$$\Sigma_{MZB} = \Delta\Delta' + D^2 + H_1H_1' + E_1^2 + 2(H_2H_2' + E_2^2),$$

$$\Sigma_{MZW} = H_1H_1' + E_1^2,$$

$$\Sigma_{DZB} = \tfrac{3}{4}(\Delta\Delta' + D^2) + H_1H_1' + E_1^2 + 2(H_2H_2' + E_2^2),$$

$$\Sigma_{DZW} = \tfrac{1}{4}(\Delta\Delta' + D^2) + H_1H_1' + E_1^2,$$

where Δ represents the loadings of the variables on the additive genetic factors, H_1 the loadings of the variables on the within-families environmental factors, and H_2 the loadings of the variables on the between-families environmental factors. D^2, E_1^2, and E_2^2 are diagonal matrices used to represent genetical and environmental influences specific to each observed variable.

The expected covariance structures given by Martin and Eaves define a confirmatory factor analysis model. A path figure for this model, where circles represent latent variables and squares observed variables, is presented in Fig. 1. In order to rewrite the expected covariance structures, a consideration of the LISREL submodel involving x variables only or, alternatively, the LISREL submodel involving y variables only would be sufficient. Clearly, one would prefer the LISREL submodel involving x variables only, as it is the more simple alternative. In this case Σ_x reduces to

$$\Sigma_x = \Lambda_x\Phi\Lambda'_x + \Theta_\delta.$$

We now can use lambda-x to represent the factor loadings on the common and specific factors and phi to represent the factor covariances. Let

$$\Lambda_x = [\Delta, H_1, H_2, D, E_1, E_2],$$

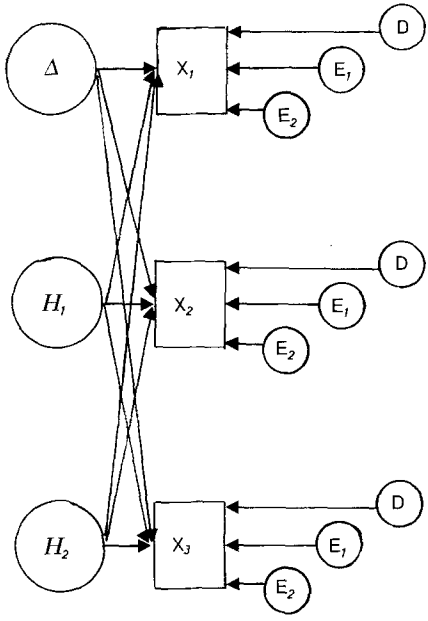

Fig. 1. LISREL confirmatory factor analysis model. Circles represent latent variables and squares represent observed variables.

in which

Δ = $q \times 1$ and contains the q loadings on the common genetic factor,

H_1 = $q \times 1$ and contains the q loadings on the within-families environmental factor,

H_2 = $q \times 1$ and contains the q loadings on the between-families environmental factor,

D = dia $q \times q$ and contains the square roots of the specific genetic variances,

E_1 = dia $q \times q$ and contains the square roots of the specific E_1 variances, and

E_2 = dia $q \times q$ and contains the square roots of the specific E_2 variances.

Lambda-x is $(q \times n)$, where $n = 3(q + 1)$ when the full model specified above is used. Phi is defined as a diagonal matrix $(n \times n)$ in which the first three diagonal elements contain the coefficients from the model specified above for, respectively, the common genetic, common E_1, and common E_2 factors. The other diagonal elements contain the coefficients for the specific variances.

To illustrate the above specifications, let $x' = [x_1, x_2, x_3]$, i.e., $q =$

3. The accommodation of the expected covariance structure is obtained by[4]

$$\text{MZB: } \Phi = \text{dia}[\ 1, 1, 2,\ \ 1,\ \ 1,\ \ 1, 1, 1, 1, 2, 2, 2],$$

$$\text{MZW: } \Phi = \text{dia}[\ 0, 1, 0,\ \ 0,\ \ 0,\ \ 0, 1, 1, 1, 0, 0, 0],$$

$$\text{DZB: } \Phi = \text{dia}\ [0.75, 1, 2, 0.75, 0.75, 0.75, 1, 1, 1, 2, 2, 2],$$

$$\text{DZW: } \Phi = \text{dia}\ [0.25, 1, 0, 0.25, 0.25, 0.25, 1, 1, 1, 0, 0, 0],$$

and lambda-x:

$$\Lambda_x = \begin{bmatrix} \delta_1 & \eta_{11} & \eta_{21} & d_1 & 0 & 0 & e_{11} & 0 & 0 & e_{21} & 0 & 0 \\ \delta_2 & \eta_{12} & \eta_{22} & 0 & d_2 & 0 & 0 & e_{12} & 0 & 0 & e_{22} & 0 \\ \delta_3 & \eta_{13} & \eta_{23} & 0 & 0 & d_3 & 0 & 0 & e_{13} & 0 & 0 & e_{23} \end{bmatrix}.$$

The four equations $\Sigma_x = \Lambda_x \Phi \Lambda'_x + \Theta_\delta$ can be fit simultaneously using a four-group design with the parameters to be estimated invariant across groups. Input matrices in LISREL for each group are the between- and within-pairs variance/covariance matrices from a multivariate analysis of variance. The number of observations (NO) equals the degrees of freedom associated with each matrix, i.e., NO equals the number of twin pairs minus one for the between matrices and the number of twin pairs for the within matrices. Since the between and the within matrices are statistically independent, we can use the chi-square test of goodness of fit of the overall model based on four independently sampled groups. Each ($q \times q$) input matrix provides $q(q + 1)/2$ unique statistics, hence the degrees of freedom for the chi-square test equal $q(q + 1)/2$ minus the number of parameters to be estimated. Note that the automatic starting values that are now available in LISREL-V and LISREL-VI cannot be used, since in general $q < n$, i.e., the number of xi factors will be greater than the number of observed x variables. However, any identified model will converge upon the same solution with whatever starting values are used.

EXAMPLE I

For illustrative purposes, simulated (5×5) matrices of mean products between and within pairs of MZ and DZ twins have been constructed (Appendix 1). The number of x variables (NX) is five, and since we are going to use the full model specified above, the number of xi factors (NK) is $3(5 + 1) = 18$. For our first examples theta delta is fixed at zero. Phi (PH) is diagonal, fixed and lambda-x (LX) is full, fixed. Next, the appro-

[4] Genetic weights are the same as used by Martin and Eaves (1977). It is also possible to use 2, 0, 1.5, and 0.5 as genetic weights. The latter set of weights gives a direct estimate of $\frac{1}{2} D_r$.

priate elements in LX are freed and specified to be invariant across groups. LISREL parameter estimates and standard errors for this model are given in Table I. LISREL-V instructions for the problem run are given in Appendix 2.

EXAMPLE II

Martin *et al.* (1981) collected data on psychomotor performance in 79 twin pairs. The twins were measured on one trial before alcohol intake and on three trials after alcohol intake. The authors give the mean product matrices between and within pairs for 21 MZ and 15 DZ female twin pairs. To analyze these data they first fitted a model with one common genetic and one common within-families environmental factor and any specific variance at each trial due to E_1 influences. This model can be analyzed with LISREL-V as follows. Let $\Lambda_x = [\Delta, H_1, E_1]$, i.e.,

$$\Lambda_x = \begin{bmatrix} \delta_0 & \eta_0 & e_0 & 0 & 0 & 0 \\ \delta_1 & \eta_1 & 0 & e_1 & 0 & 0 \\ \delta_2 & \eta_2 & 0 & 0 & e_2 & 0 \\ \delta_3 & \eta_3 & 0 & 0 & 0 & e_3 \end{bmatrix}.$$

Table I. LISREL Parameter Estimates (Example I): Δ, H_1 and H_2 Represent Factor Loadings and D, E_1, and E_2 Are Square Roots of the Specific Variances

	Δ	D	H_1	E_1	H_2	E_2
			LISREL estimates			
X_1	10.001	7.776	8.888	5.921	13.764	3.725
X_2	12.660	8.520	8.015	7.948	14.174	5.268
X_3	14.961	7.005	7.026	8.003	7.042	4.928
X_4	12.992	5.882	6.006	8.153	6.933	6.536
X_5	10.006	9.296	4.961	6.062	7.009	4.749
			$\chi_{30}^2 = 1.69$			
			Standard errors			
X_1	1.232	1.043	0.291	0.234	0.645	1.271
X_2	1.234	1.245	0.312	0.218	0.699	1.047
X_3	0.905	1.542	0.298	0.205	0.667	0.884
X_4	0.820	1.713	0.286	0.198	0.594	0.635
X_5	0.707	0.734	0.223	0.154	0.478	0.634

The expected covariance structure for MZB, etc., can be obtained along the lines described previously.

$$\text{MZB: } \Phi = \text{dia}\,[\ \ 1, 1, 1, 1, 1, 1].$$

$$\text{MZW: } \Phi = \text{dia}\,[\ \ 0, 1, 1, 1, 1, 1, 1].$$

$$\text{DZB: } \Phi = \text{dia}\,[0.75, 1, 1, 1, 1, 1, 1].$$

$$\text{DZW: } \Phi = \text{dia}\,[0.25, 1, 1, 1, 1, 1, 1].$$

To run this analysis with LISREL-V, one specifies NX = 4, NK = 6, TD = ZE, PH = DI, FI, and LX = FU, FI. LISREL gave a chi-square of 31.21 (df = 28, P = 0.31) for this model; the chi-square obtained by Martin *et al.* was 33.27.

In a second analysis a second common genetic factor independent of the first one was fit, with loadings on the last three trials (after alcohol) but not on the first trial. The lambda-x and phi matrices now become

$$\Lambda_x = [\Delta_1, \Delta_2, H_1, E_1], \text{ i.e.,}$$

$$\Lambda_x = \begin{bmatrix} \delta_{10} & — & \eta_0 & e_0 & 0 & 0 & 0 \\ \delta_{11} & \delta_{21} & \eta_1 & 0 & e_1 & 0 & 0 \\ \delta_{12} & \delta_{22} & \eta_2 & 0 & 0 & e_2 & 0 \\ \delta_{13} & \delta_{23} & \eta_3 & 0 & 0 & 0 & e_3 \end{bmatrix}.$$

$$\text{MZB: } \Phi = \text{dia}\,[\ \ 1,\ \ \ 1, 1, 1, 1, 1, 1].$$

$$\text{MZW: } \Phi = \text{dia}\,[\ \ 0,\ \ \ 0, 1, 1, 1, 1, 1].$$

$$\text{DZB: } \Phi = \text{dia}\,[0.75, 0.75, 1, 1, 1, 1, 1].$$

$$\text{DZW: } \Phi = \text{dia}\,[0.25, 0.25, 1, 1, 1, 1, 1].$$

Table II. LISREL Estimates (Example II)

	Δ_1	Δ_2	H_1	E_1
T_0	20.250	—	5.471	6.039
T_1	13.790	5.588	8.461	4.891
T_2	16.781	5.925	7.529	7.229
T_3	16.481	5.980	6.268	6.395
		$\chi_{25}^2 = 28.87$		

Table III. Full $D_1E_1E_2$ Model Fitted to the Loehlin and Vandenberg (1968) Data (Example III)

	Δ	D	H_1	E_1	H_2	E_2
			LISREL estimates			
N	50.917	20.900	1.170	19.198	19.487	1.342
V	16.806	17.099	10.222	7.798	26.693	0.428
S	31.001	37.599	2.111	21.099	11.906	27.500
W	14.681	22.900	6.569	12.700	12.475	0.425
R	14.461	1.582	6.652	8.799	14.726	11.398
			$\chi_{30}^2 = 32.65$			
			Estimates of Martin and Eaves (1977)			
N	50.897	20.972	1.159	19.216	19.463	1.761
V	16.830	17.114	10.201	7.821	26.662	2×10^{-6}
S	31.027	37.647	2.123	21.094	11.918	27.504
W	14.686	22.926	6.580	12.706	12.453	1×10^{-5}
R	14.451	1.628	6.629	8.853	14.720	11.414
			$\chi_{30}^2 = 33.0$			

Lambda-x is thus 4 × 7 and phi is 7 × 7. LISREL parameters estimates and chi-square are given in Table II. The chi-square for this model obtained by Martin *et al.* was 30.82.

EXAMPLE III

For our third example we used twin data published by Loehlin and Vandenberg (1968) on five of Thurstone's Primary Mental Abilities (Number, Verbal, Space, Word Fluency, and Reasoning).[5]

Martin and Eaves fitted several models to these data. First, a D_RE_1 model containing a common genetic factor, a within-families environmental factor, and specific genetic and specific within-families influences is considered. The accommodation to LISREL of this model is obtained by

$$\Lambda_x = [\Delta, H_1, D, E_1].$$

Second, an E_1E_2 model containing a within-families environmental factor,

[5] Note that in the DZW matrix rows 3 and 4 have been switched (Loehlin and Vandenberg, 1968, p. 281).

a between-families environmental factor, and specific within- and between families environmental influences is fit:

$$\Lambda_x = [H_1, H_2, E_1, E_2].$$

Third, a $D_R E_1 E_2$ model containing a common genetic factor, a common within-families environmental factor, and a common between-families environmental factor, plus specific genetic, within-families, and between-families environmental influences is considered. This is the full model that was introduced above.

We used LISREL to reanalyze these models and found that, in all cases, the LISREL parameter estimates were very close to the estimates obtained by Martin and Eaves. Table III presents the LISREL parameter estimates for the full $D_R E_1 E_2$ model and the estimates obtained by Martin and Eaves.

To look at the possible effects of assortative mating, Martin and Eaves also fit the full $D_R E_1 E_2$ model in which the common genetic factor Δ and the between-families environmental factor H_2 have loadings which are constrained to be related by a scalar constant b: $H_2 = b\Delta$. In order to accommodate this constrained $D_R E_1 E_2$ model to LISREL, we introduce the following redefinition:

$$\Lambda_x = [\Delta, H_1, \Delta, D, E_1, E_2],$$

expressing the constraint that the factor loadings on Δ are equal to those on H_2. Up until now all elements in the matrix phi have been fixed at known coefficients from the twin model specified above. In contrast, element (3,3) in phi is now freed, whereby the equality of the factor loadings of Δ and H_2 as expressed by lambda-x is reduced to a proportionality. Note that

$$\Sigma_{MZB} = \Delta\Delta' + D^2 + H_1 H_1' + E_1^2 + 2(H_2 H_2' + E_2^2),$$

$$\Sigma_{DZB} = \tfrac{3}{4}(\Delta\Delta' + D^2) + H_1 H_1' + E_1^2 + 2(H_2 H_2' + E_2^2),$$

that is, phi(3,3) = $2b$. The LISREL estimate of b thus obtained was 0.6, which is close to the estimate of 0.7 obtained by Martin and Eaves.

EXAMPLE IV

In LISREL specific variances usually are represented by Θ. However, the model we have been using contains various specific variances, viz., D^2, E_1^2, and E_2^2, that compelled a different approach in which in each specific variance was conceived of as a distinct latent factor. Con-

Table IV. LISREL Estimates (Example IV)

	Δ	D	H_1	E_1	H_2	E_2
X_1	10.042	7.051	9.003	6.000	14.011	3.992
X_2	13.018	8.998	8.003	8.008	13.998	5.032
X_3	15.017	7.094	6.998	8.001	6.999	5.076
X_4	13.017	7.074	6.000	8.003	7.001	6.053
X_5	10.014	8.999	5.001	6.000	7.003	5.000

Measurement errror variances

TD1	TD2	TD3	TD4	TD5
25.0	25.0	49.0	25.0	25.0

$\chi_{185}^2 = 0.23$

sequently, Θ_δ was fixed at zero. In contrast, we could have treated specific E_1 variances differently by representing these in terms of Θ_δ. This would have shown more clearly that E_1 variances are confounded with measurement error variance. Notice that the assignment of any measurement error variance present to E_1 is inherent to the genetic model and not to the corresponding LISREL model. Hence, while treating specific E_1 variances as we do, i.e., as being due to distinct latent factors, one still cannot use theta delta to obtain separate estimates of measurement error variance without the invocation of additional structure, such as a repeated-measures design.

As a last example we simulated a repeated-measures twin design, in which five variables are measured twice. We now have four (10 × 10) observed covariance matrices (Appendix 3) and can estimate the variance associated with measurement errors in any of the five variables in theta delta. For this analysis the factor loadings on the common and specific factors are constrained to be invariant over testing sessions. That is, the first five loadings on the xi factors are equal to the second five factor loadings. Likewise, the variances in theta delta are constrained to be equal over testing sessions. This model can be defined as follows: NX = 10, NK = 18, LX = FU, FI, PH = DI, FI, and TD = DI, FI. Next, the appropriate elements in LX and TD are freed and specified to be invariant over groups and testing sessions. LISREL estimates of factor loadings and error variances are given in Table IV. For the third variable the total variance is 374.7 and the error variance (TD3) is 49.0. This means that 13.1% of the total variance can be explained by measurement error.

DISCUSSION

The method of Martin and Eaves and the LISREL approach are equivalent. This is a pleasing state of affairs, as LISREL is easy of access and well-known, whence the genetic analysis of covariance structure might gain in impetus. In fact, the LISREL approach can be used whenever an explanation of observed covariance matrices, e.g., of relatives, in terms of genetic and environmental components is at stake.

Our method is one of several approaches to use LISREL for the genetic analysis of covariance structure (Fulker *et al.*, 1983; Cantor, 1983). Fulker *et al.* (1983), using an approach similar to that outlined here, employed LISREL confirmatory factor analysis to examine the genetic and environmental covariance structure of data on income, occupation, and schooling. Cantor (1983) used the LISREL confirmatory factor analysis for the genetic analysis of ridge count data from the offspring of monozygotic twins. In her approach the theta matrix is used to estimate

Appendix 1. Input Matrices (Example I)

MZ between

683.648				
588.149	819.467			
403.527	444.460	535.363		
375.741	410.954	335.323	486.632	
337.608	363.624	282.018	257.372	385.213

MZ within

114.054				
71.265	127.780			
62.397	56.472	113.704		
53.185	48.135	42.146	102.091	
44.052	39.869	34.908	29.755	61.120

DZ between

638.284				
556.119	758.444			
369.790	400.248	465.354		
339.667	366.791	284.565	437.188	
312.019	333.919	247.405	224.013	349.307

DZ within

154.429				
102.845	184.739			
100.080	103.196	180.921		
86.475	89.091	90.564	154.025	
69.260	71.162	72.193	62.291	108.606

Appendix 2. LISREL Control Cards (Example I)

Group 1. MZ between

```
DA NG=4 NI=5 NO=999 MA=CM
CM SY
MO NX=5 NK=18 PH=DI,FI LX=FU,FI TD=ZE
ST 1.0 PH(1,1) PH(4,4) PH(5,5) PH(6,6) PH(7,7) PH(8,8)
ST 1.0 PH(2,2) PH(9,9) PH(10,10) PH (11,11) PH(12,12) PH(13,13)
ST 2.0 PH(3,3) PH(14,14) PH(15,15) PH(16,16) PH(17,17) PH(18,18)
FR LX(1,1) LX(2,1) LX(3,1) LX(4,1) LX(5,1)
FR LX(1,2) LX(2,2) LX(3,2) LX(4,2) LX(5,2)
FR LX(1,3) LX(2,3) LX(3,3) LX(4,3) LX(5,3)
FR LX(1,4) LX(2,5) LX(3,6) LX(4,7) LX(5,8)
FR LX(1,9) LX(2,10) LX(3,11) LX(4,12) LX(5,13)
FR LX(1,14) LX(2,15) LX(3,16) LX(4,17) LX(5,18)
ST 20 ALL
OU SE NS TO
```

Group 2. MZ within

```
DA NO=1000
CM SY
MO NX=5 NK=18 PH=PS LX=IN TD=ZE
ST 0.0 PH(1,1) PH(4,4) PH(5,5) PH(6,6) PH(7,7) PH(8,8)
ST 1.0 PH(2,2) PH(9,9) PH(10,10) PH(11,11) PH(12,12) PH(13,13)
ST 0.0 PH(3,3) PH(14,14) PH(15,15) PH(16,16) PH(17,17) PH(18,18)
OU TO
```

Group 3. DZ between

```
DA NO=999
CM SY
MO NX=5 NK=18 PH=PS LX=IN TD=ZE
ST 0.75 PH(1,1) PH(4,4) PH(5,5) PH(6,6) PH(7,7) PH(8,8)
ST 1.0 PH(2,2) PH(9,9) PH(10,10) PH(11,11) PH(12,12) PH(13,13)
ST 2.0 PH(3,3) PH(14,14) PH(15,15) PH(16,16) PH(17,17) PH(18,18)
OU TO
```

Group 4. DZ within

```
DA NO=1000
CM SY
MO NX=5 NK=18 PH=PS LK=IN TD=ZE
ST 0.25 PH(1,1) PH(4,4) PH(5,5) PH(6,6) PH(7,7) PH(8,8)
ST 1.0 PH(2,2) PH(9,9) PH(10,10) PH(11,11) PH(12,12) PH(13,13)
ST 0.0 PH(3,3) PH(14,14) PH(15,15) PH(16,16) PH(17,17) PH(18,18)
OU TO
```

Appendix 3. Input Matrices (Example IV)

MZ between

715.00									
594.00	845.00								
409.00	447.00	584.00							
380.00	413.00	335.00	513.00						
341.00	366.00	283.00	258.00	415.00					
690.00	594.00	409.00	380.00	341.00	715.00				
594.00	820.00	447.00	413.00	366.00	594.00	845.00			
409.00	447.00	535.00	335.00	283.00	409.00	447.00	584.00		
380.00	413.00	335.00	488.00	258.00	380.00	413.00	335.00	513.00	
341.00	366.00	283.00	258.00	390.00	341.00	366.00	283.00	258.00	415.00

MZ within

142.00									
72.00	153.00								
63.00	56.00	162.00							
54.00	48.00	42.00	125.00						
45.00	40.00	35.00	30.00	86.00					
117.00	72.00	63.00	54.00	45.00	142.00				
72.00	128.00	56.00	48.00	40.00	72.00	153.00			
63.00	56.00	113.00	42.00	35.00	63.00	56.00	162.00		
54.00	48.00	42.00	100.00	30.00	54.00	48.00	42.00	125.00	
45.00	40.00	35.00	30.00	61.00	45.00	40.00	35.00	30.00	86.00

DZ between

677.75									
561.50	782.50								
371.50	398.25	515.50							
347.50	370.75	286.25	458.50						
316.00	333.50	245.50	225.50	369.75					
652.75	561.50	371.50	347.50	316.00	677.75				
561.50	757.50	398.25	370.75	333.50	561.50	782.50			
371.50	398.25	466.50	286.25	245.50	371.50	398.25	515.50		
347.50	370.75	286.25	433.50	225.50	347.50	370.75	286.25	458.50	
316.00	333.50	245.50	225.50	344.75	316.00	333.50	245.50	225.50	369.75

DZ within

179.25									
104.50	215.50								
100.50	104.75	230.50							
86.50	90.25	90.75	179.50						
70.00	72.50	72.50	62.50	131.25					
154.25	104.50	100.50	86.50	70.00	179.25				
104.50	190.50	104.75	90.25	72.50	104.50	215.50			
100.50	104.75	181.50	90.75	72.50	100.50	104.75	230.50		
86.50	90.25	90.75	154.50	62.50	86.50	90.25	90.75	179.50	
70.00	72.50	72.50	62.50	106.25	70.00	72.50	72.50	62.50	131.25

residual variances that cannot be accounted for by the postulated factors. These specific residual variances necessarily represent E_1 influences and thus are confounded with other specific variances, if present. Specific variances, however, can be represented as distinct latent factors as in our examples. As a consequence, in studies in which information on the test–retest reliabilities of the measures is available, the theta matrix can be used as the matrix of variances of measurement errors.

The LISREL approach not only is equivalent to the method used by Martin and Eaves, but also can be used to explore more elaborate models. For instance, in a longitudinal analysis it is possible to obtain functional relationships between genetic and/or environmental covariance structures at consecutive time points. A particular simple example would be a proportional relationship between factor loadings within or between consecutive occasions. In fact, we have invoked such a within-occasion proportional relationship in our example in which the Δ and the H_2 factor loadings were related by a scalar constant b. One other feature of LISREL is the option to test the assumption of unequal means for the latent factors. This might be useful in the analysis of parent–offspring data where parents and children may have different means on certain variables, in the analysis of sex differences, or again, in a longitudinal analysis.

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